WHAT IS CLAIMED IS:

1. A composition of matter that comprises a library of analytes, said analytes being hybridized to an array of nucleic acids, said nucleic acids being fixed or immobilized to a solid support, wherein said analytes comprise an inherent universal detection target (UDT), and a universal detection element (UDE) attached to said UDT wherein said UDE generates a signal indicating the presence or quantity of said analytes, or said attachment of UDE to UDT.

2. The composition of claim 1, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

3. The composition of claim 1, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

4. The composition of claim 1, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

5. The composition of claim 4, wherein said analogs comprise PNA.

6. The composition of claims 4 or 5, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

7. The composition of claim 1, wherein said solid support is porous or non-porous.

8. The composition of claim 7, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

9. The composition of claim 7, wherein said non-porous solid support comprises glass or plastic.

10. The composition of claim 1, wherein said solid support is transparent, translucent, opaque or reflective.

11. The composition of claim 1, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

12. The composition of claim 11, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

13. The composition of claim 1, wherein said inherent UDT is selected from the group consisting of 3′ polyA segments, 5′ caps, secondary structures, consensus sequences and a combination of any of the foregoing.

14. The composition of claim 13, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats and a combination of any of the foregoing.

15. The composition of claim 1, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs, polypeptides, polysaccharides, synthetic polymers and a combination of any of the foregoing.

16. The composition of claim 4, wherein said analogs comprise PNA.

17. The composition of claim 1, wherein said UDE generates a signal directly or indirectly.

18. The composition of claim 17, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

19. The composition of claim 17, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

20. The composition of claim 19, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

21. A composition of matter that comprises a library of analytes, said analytes being hybridized to an array of nucleic acids, said nucleic acids being fixed or immobilized to a solid support, wherein said analytes comprise a non-inherent universal detection target (UDT) and a universal detection element (UDE) hybridized to said UDT, wherein said UDE generates a signal directly or indirectly to detect the presence or quantity of said analytes.

22. The composition of claim 21, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

23. The composition of claim 21, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

24. The composition of claim 21, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

25. The composition of claim 24, wherein said analogs comprise PNA.

26. The composition of claims 24 or 25, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

27. The composition of claim 21, wherein said solid support is porous or non-porous.

28. The composition of claim 27, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

29. The composition of claim 27, wherein said non-porous solid support comprises glass or plastic.

30. The composition of claim 21, wherein said solid support is transparent, translucent, opaque or reflective.

31. The composition of claim 21, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

32. The composition of claim 31, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

33. The composition of claim 21, wherein said non-inherent universal detection target (UDT) comprises homopolymeric sequences.

34. The composition of claim of 21, wherein said non-inherent universal detection target (UDT) comprises heteropolymeric sequences.

35. The composition of claim 21, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

36. The composition of claim 35, wherein said analogs comprise PNA.

37. The composition of claim 21, wherein said UDE generates a signal directly or indirectly.

38. The composition of claim 37, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

39. The composition of claim 37, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

40. The composition of claim 39, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

41. A composition of matter that comprises a library of analytes, said analytes being hybridized to an array of nucleic acids, said nucleic acids being fixed or immobilized to a solid support, wherein said hybridization between said analytes and said nucleic acids generate a domain for complex formation, and said composition further comprising a signaling entity complexed to said domain.

42. The composition of claim 41, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

43. The composition of claim 41, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

44. The composition of claim 41, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

45. The composition of claim 44, wherein said analogs comprise PNA.

46. The composition of claims 44 or 45, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

47. The composition of claim 41, wherein said solid support is porous or non-porous.

48. The composition of claim 47, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

49. The composition of claim 47, wherein said non-porous solid support comprises glass or plastic.

50. The composition of claim 41, wherein said solid support is transparent, translucent, opaque or reflective.

51. The composition of claim 41, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

52. The composition of claim 41, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

53. The composition of claim 41, wherein said domain for complex formation is selected from the group consisting of DNA-DNA hybrids, DNA-RNA hybrids, RNA-RNA hybrids, DNA-PNA hybrids and RNA-PNA hybrids.

54. The composition of claim 41, wherein said signaling entity complexed to said domain is selected from the group consisting of proteins and intercalators.

55. The composition of claim 54, wherein said proteins comprise nucleic acid binding proteins which bind preferentially to double-stranded nucleic acid.

56. The composition of claim 55, wherein said nucleic acid binding proteins comprise antibodies.

57. The composition of claim 56, wherein said antibodies are specific for nucleic acid hybrids selected from the group consisting of DNA-DNA hybrids, DNA-RNA hybrids, RNA-RNA hybrids, DNA-PNA hybrids and RNA-PNA hybrids

58. The composition of claim 54, wherein said intercalators are selected from the group consisting of ethidium bromide, diethidium bromide, acridine orange and SYBR Green.

59. The composition of claim 41, wherein said proteins generate a signal directly or indirectly.

60. The composition of claim 59, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron

dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

61. The composition of claim 59, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

62. The composition of claim 61, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

63. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified, wherein each of said nucleic acids of interest comprise at least one inherent universal detection target (UDT); and

(iii) universal detection elements (UDE) which generates a signal directly or indirectly;

b) hybridizing said library (ii) with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

c) contacting said UDEs with said UDTs to form a complex bound to said array;

d) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

64. The process of claim 63, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

65. The process of claim 64, wherein said analogs comprise PNA.

66. The process of claims 64 or 65, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

67. The process of claim 63, wherein said solid support is porous or non-porous.

68. The process of claim 67, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

69. The process of claim 67, wherein said non-porous solid support comprises glass or plastic.

70. The process of claim 63, wherein said solid support is transparent, translucent, opaque or reflective.

71. The process of claim 63, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

72. The process of claim 71, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

73. The process of claim 63, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

74. The process of claim 63, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

75. The process of claim 63, wherein said inherent UDT is selected from the group consisting of 3′ polyA segments, 5′ caps, secondary structures, consensus sequences, and a combination of any of the foregoing.

76. The process of claim 75, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

77. The process of claim 63, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs, polypeptides, polysaccharides, synthetic polymers and a combination of any of the foregoing.

78. The process of claim 64, wherein said analogs comprise PNA.

79. The process of claim 63, wherein said UDE generates a signal directly or indirectly.

80. The process of claim 79, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

81. The process of claim 79, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

82. The process of claim 81, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

83. The process of claim 63, comprising one or more washing steps.

84. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified, wherein each of said nucleic acids of interest comprise at least one inherent universal detection target (UDT); and

(iii) universal detection elements (UDE) which generates a signal directly or indirectly;

b) contacting said UDEs with said UDTs in said library of nucleic acid analytes to form one or more complexes;

c) hybridizing said library of nucleic acid analytes with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

d) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

85. The process of claim 84, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

86. The process of claim 85, wherein said analogs comprise PNA.

87. The process of claims 85 or 86, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

88. The process of claim 84, wherein said solid support is porous or non-porous.

89. The process of claim 88, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

90. The process of claim 88, wherein said non-porous solid support comprises glass or plastic.

91. The process of claim 84, wherein said solid support is transparent, translucent, opaque or reflective.

92. The process of claim 84, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

93. The process of claim 92, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

94. The process of claim 84, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

95. The process of claim 84, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

96. The process of claim 84, wherein said inherent UDT is selected from the group consisting of 3′ polyA segments, 5′ caps, secondary structures, consensus sequences, and a combination of any of the foregoing.

97. The process of claim 96, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

98. The process of claim 84, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs, polypeptides, polysaccharides, synthetic polymers and a combination of any of the foregoing.

99. The process of claim 98, wherein said analogs comprise PNA.

100. The process of claim 84, wherein said UDE generates a signal directly or indirectly.

101. The process of claim 100, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

102. The process of claim 100, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

103. The process of claim 102, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

104. The process of claim 84, comprising one or more washing steps.

105. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified, wherein each of said nucleic acids of interest comprise at least one non-inherent universal detection target (UDT), wherein said non-inherent UDT is attached to said nucleic acid analytes; and

(iii) universal detection elements (UDE) which generate a signal directly or indirectly;

b) hybridizing said library (ii) with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

c) contacting said UDEs with said UDTs to form a complex bound to said array;

d) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

106. The process of claim 105, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

107. The process of claim 106, wherein said analogs comprise PNA.

108. The process of claims 106 or 107, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

109. The process of claim 105, wherein said solid support is porous or non-porous.

110. The process of claim 109, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

111. The process of claim 109, wherein said non-porous solid support comprises glass or plastic.

112. The process of claim 105, wherein said solid support is transparent, translucent, opaque or reflective.

113. The process of claim 105, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

114. The process of claim 113, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

115. The process of claim 105, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

116. The process of claim 105, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

117. The process of claim 105, wherein said non-inherent universal detection target (UDT) comprises homopolymeric sequences.

118. The process of claim of 105, wherein said non-inherent universal detection target (UDT) comprises heteropolymeric sequences.

119. The process of claim 105, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

120. The process of claim 119, wherein said analogs comprise PNA.

121. The process of claim 105, wherein said UDE generates a signal directly or indirectly.

122. The process of claim 121, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

123. The process of claim 121, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

124. The process of claim 123, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

125. The process of claim 105, comprising one or more washing steps.

126. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified, wherein each of said nucleic acids of interest comprise at least one non-inherent universal detection target (UDT), wherein said non-inherent UDTs are attached to said nucleic acid analytes; and

(iii) universal detection elements (UDE) which generate a signal directly or indirectly;

b) contacting said UDEs with said UDTs in said library of nucleic acid analytes to form one or more complexes;

c) hybridizing said library (ii) with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

d) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

127. The process of claim 126, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

128. The process of claim 127, wherein said analogs comprise PNA.

129. The process of claims 127 or 128, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

130. The process of claim 126, wherein said solid support is porous or non-porous.

131. The process of claim 130, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

132. The process of claim 130, wherein said non-porous solid support comprises glass or plastic.

133. The process of claim 126, wherein said solid support is transparent, translucent, opaque or reflective.

134. The process of claim 126, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

135. The process of claim 134, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

136. The process of claim 126, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

137. The process of claim 126, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

138. The process of claim 126, wherein said non-inherent universal detection target (UDT) comprises homopolymeric sequences.

139. The process of claim of 126, wherein said non-inherent universal detection target (UDT) comprises heteropolymeric sequences.

140. The process of claim 126, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

141. The process of claim 140, wherein said analogs comprise PNA.

142. The process of claim 126, wherein said UDE generates a signal directly or indirectly.

143. The process of claim 142, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

144. The process of claim 142, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

145. The process of claim 144, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

146. The process of claim 126, comprising one or more washing steps.

147. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) means for attaching one or more universal detection targets (UDT) to a nucleic acid;

(iv) universal detection elements (UDE) which generates a signal directly or indirectly;

b) attaching said UDTs (iii) to said library of nucleic acid analytes (ii);

c) hybridizing said library (ii) with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

d) contacting said UDEs with said UDTs to form a complex bound to said array;

e) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

148. The process of claim 147, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

149. The process of claim 148, wherein said analogs comprise PNA.

150. The process of claims 148 or 149, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

151. The process of claim 147, wherein said solid support is porous or non-porous.

152. The process of claim 151, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

153. The process of claim 151, wherein said non-porous solid support comprises glass or plastic.

154. The process of claim 147, wherein said solid support is transparent, translucent, opaque or reflective.

155. The process of claim 147, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

156. The process of claim 155, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

157. The process of claim 147, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

158. The process of claim 147, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

159. The process of claim 147, wherein said attaching means add homopolymeric sequences through an enzyme selected from the group consisting of poly A polymerase and terminal transferase.

160. The process of claim 147, wherein said attaching means add homopolymeric or heteropolymeric sequences through an enzyme selected from the group consisting of DNA ligase and RNA ligase.

161. The process of claim 147, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

162. The process of claim 161, wherein said analogs comprise PNA.

163. The process of claim 147, wherein said UDE generates a signal directly or indirectly.

164. The process of claim 163, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

165. The process of claim 163, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

166. The process of claim 165, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

167. The process of claim 147, comprising one or more washing steps.

168. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) means for attaching one or more universal detection targets (UDT) to a nucleic acid;

(iv) universal detection elements (UDE) which generates a signal directly or indirectly;

b) attaching said UDTs (iii) to said library of nucleic acid analytes (ii);

c) contacting said UDEs with said UDTs in said library of nucleic acid analytes to form one or more complexes;

d) hybridizing said library (ii) with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

e) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

169. The process of claim 168, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

170. The process of claim 169, wherein said analogs comprise PNA.

171. The process of claims 169 or 170, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

172. The process of claim 168, wherein said solid support is porous or non-porous.

173. The process of claim 172, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

174. The process of claim 172, wherein said non-porous solid support comprises glass or plastic.

175. The process of claim 168, wherein said solid support is transparent, translucent, opaque or reflective.

176. The process of claim 168, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

177. The process of claim 176, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

178. The process of claim 168, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

179. The process of claim 168, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

180. The process of claim 168, wherein said attaching means add homopolymeric sequences through an enzyme selected from the group consisting of poly A polymerase and terminal transferase.

181. The process of claim 168, wherein said attaching means add homopolymeric or heteropolymeric sequences through an enzyme selected from the group consisting of DNA ligase and RNA ligase.

182. The process of claim 168, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

183. The process of claim 182, wherein said analogs comprise PNA.

184. The process of claim 168, wherein said UDE generates a signal directly or indirectly.

185. The process of claim 184, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

186. The process of claim 184, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

187. The process of claim 186, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

188. The process of claim 168, comprising one or more washing steps.

189. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified; and

(iii) universal detection elements (UDEs) which bind to a domain formed by nucleic acid hybrids for complex formation and generate a signal directly or indirectly;

b) hybridizing said library (ii) with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present, wherein said formed hybrids generate a domain for complex formation;

c) contacting said UDEs with said hybrids to form a complex bound to said array;

d) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

190. The process of claim 189, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

191. The process of claim 190, wherein said analogs comprise PNA.

192. The process of claims 190 or 191, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

193. The process of claim 189, wherein said solid support is porous or non-porous.

194. The process of claim 193, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

195. The process of claim 193, wherein said non-porous solid support comprises glass or plastic.

196. The process of claim 189, wherein said solid support is transparent, translucent, opaque or reflective.

197. The process of claim 189, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

198. The process of claim 197, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

199. The process of claim 189, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

200. The process of claim 189, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

201. The process of claim 189, wherein said domain for complex formation is selected from the group consisting of DNA-DNA hybrids, DNA-RNA hybrids, RNA-RNA hybrids, DNA-PNA hybrids and RNA-PNA hybrids.

202. The process of claim 189, wherein said signaling entity complexed to said domain is selected from the group consisting of proteins and intercalators.

203. The process of claim 202, wherein said proteins comprise nucleic acid binding proteins which bind preferentially to double-stranded nucleic acid.

204. The process of claim 203, wherein said nucleic acid binding proteins comprise antibodies.

205. The process of claim 204, wherein said antibodies are specific for nucleic acid hybrids selected from the group consisting of DNA-DNA hybrids, DNA-RNA hybrids, RNA-RNA hybrids, DNA-PNA hybrids and RNA-PNA hybrids.

206. The process of claim 202, wherein said intercalators are selected from the group consisting of ethidium bromide, diethidium bromide, acridine orange and SYBR Green.

207. The process of claim 189, wherein said proteins generate a signal directly or indirectly.

208. The process of claim 207, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

209. The process of claim 207, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

210. The process of claim 209, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

211. The process of claim 189, further comprising one or more washing steps.

212. A composition of matter comprising a library of first nucleic acid analyte copies, said first nucleic acid copies being hybridized to an array of nucleic acids, said nucleic acids being fixed or immobilized to a solid support, wherein said first nucleic acid copies comprise an inherent universal detection target (UDT) and a universal detection element (UDE) attached to said UDT, wherein said UDE generates a signal directly or indirectly to detect the presence or quantity of said analytes.

213. The composition of claim 212, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

214. The composition of claim 212, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

215. The composition of claim 212, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

216. The composition of claim 215, wherein said analogs comprise PNA.

217. The composition of claims 215 or 216, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

218. The composition of claim 212, wherein said solid support is porous or non-porous.

219. The composition of claim 218, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

220. The composition of claim 218, wherein said non-porous solid support comprises glass or plastic.

221. The composition of claim 212, wherein said solid support is transparent, translucent, opaque or reflective.

222. The composition of claim 212, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

223. The composition of claim 222, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

224. The composition of claim 212, wherein said inherent UDT is selected from the group consisting of poly T segments, secondary structures, consensus sequences, and a combination of any of the foregoing.

225. The composition of claim 224, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

226. The composition of claim 212, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs, polypeptides, polysaccharides, synthetic polymers and a combination of any of the foregoing.

227. The composition of claim 226, wherein said analogs comprise PNA.

228. The composition of claim 212, wherein said UDE generates a signal directly or indirectly.

229. The composition of claim 228, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

230. The composition of claim 228, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

231. The composition of claim 230, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

232. A composition of matter comprising a library of first nucleic acid copies, said first nucleic acid copies being hybridized to an array of nucleic acids, said nucleic acids being fixed or immobilized to a solid support, wherein said first nucleic acid copies comprise one or more non-inherent universal detection targets (UDTs) and one or more universal detection elements (UDEs) attached to said UDTs, wherein said UDEs generate a signal directly or indirectly to detect the presence or quantity of said analytes, and wherein said UDTs are either: (i) at the 5' ends of said first nucleic acid copies and not adjacent to an oligoT segment or sequence, or (ii) at the 3' ends of said first nucleic acid copies, or (iii) both (i) and (ii).

233. The composition of claim 232, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

234. The composition of claim 232, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

235. The composition of claim 232, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

236. The composition of claim 235, wherein said analogs comprise PNA.

237. The composition of claims 235 or 236, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

238. The composition of claim 232, wherein said solid support is porous or non-porous.

239. The composition of claim 238, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

240. The composition of claim 238, wherein said non-porous solid support comprises glass or plastic.

241. The composition of claim 232, wherein said solid support is transparent, translucent, opaque or reflective.

242. The composition of claim 232, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

243. The composition of claim 242, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

244. The composition of claim 232, wherein said non-inherent universal detection target (UDT) comprises homopolymeric sequences.

245. The composition of claim of 232, wherein said non-inherent universal detection target (UDT) comprises heteropolymeric sequences.

246. The composition of claim 232, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs, polypeptides, polysaccharides, synthetic polymers and a combination of any of the foregoing.

247. The composition of claim 246, wherein said analogs comprise PNA.

248. The composition of claim 232, wherein said UDE generates a signal directly or indirectly.

249. The composition of claim 248, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

250. The composition of claim 248, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

251. The composition of claim 250, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

252. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical in part or whole to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified, wherein each of said nucleic acids of interest comprise at least one inherent universal detection target (UDT);

(iii) universal detection elements (UDE) which generate a signal directly or indirectly; and

(iv) polymerizing means for synthesizing nucleic acid copies of said nucleic acids of analytes;

b) synthesizing one or more first nucleic acid copies which are complementary to all or part of said nucleic acid analytes and synthesizing sequences which are complementary to all or part of said UDT to form a complementary UDT;

c) hybridizing said first nucleic acid copies with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

d) contacting said UDEs with said complementary UDTs of said first nucleic acid copies to form a complex bound to said array;

e) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

253. The process of claim 252, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

254. The process of claim 253, wherein said analogs comprise PNA.

255. The process of claims 253 or 254, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

256. The process of claim 252, wherein said solid support is porous or non-porous.

257. The process of claim 256, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

258. The process of claim 256, wherein said non-porous solid support comprises glass or plastic.

259. The process of claim 252, wherein said solid support is transparent, translucent, opaque or reflective.

260. The process of claim 252, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

261. The process of claim 260, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

262. The process of claim 252, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

263. The process of claim 252, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

264. The process of claim 252, wherein said inherent UDT is selected from the group consisting of poly T segments, secondary structures, consensus sequences, and a combination of any of the foregoing.

265. The process of claim 264, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

266. The process of claim 252, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs, polypeptides, polysaccharides, synthetic polymers and a combination of any of the foregoing.

267. The process of claim 266, wherein said analogs comprise PNA.

268. The process of claim 252, wherein said UDE generates a signal directly or indirectly.

269. The process of claim 268, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

270. The process of claim 268, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

271. The process of claim 270, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

272. The process of claim 252, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

273. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical in part or whole to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified, wherein each of said nucleic acids of interest comprise at least one inherent universal detection target (UDT);

(iii) universal detection elements (UDE) which generate a signal directly or indirectly; and

(iv) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes;

b) synthesizing one or more first nucleic acid copies of said nucleic acid analytes;

c) contacting said UDEs with said UDTs in said first nucleic acid copies to form one or more complexes;

d) hybridizing said first nucleic acid copies with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present; and

e) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

274. The process of claim 273, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

275. The process of claim 274, wherein said analogs comprise PNA.

276. The process of claims 274 or 275, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

277. The process of claim 273, wherein said solid support is porous or non-porous.

278. The process of claim 277, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

279. The process of claim 277, wherein said non-porous solid support comprises glass or plastic.

280. The process of claim 273, wherein said solid support is transparent, translucent, opaque or reflective.

281. The process of claim 273, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

282. The process of claim 281, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

283. The process of claim 273, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

284. The process of claim 273, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

285. The process of claim 273, wherein said inherent UDT is selected from the group consisting of poly T segments, secondary structures, consensus sequences, and a combination of any of the foregoing.

286. The process of claim 285, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

287. The process of claim 273, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs, polypeptides, polysaccharides, synthetic polymers and a combination of any of the foregoing.

288. The process of claim 287, wherein said analogs comprise PNA.

289. The process of claim 273, wherein said UDE generates a signal directly or indirectly.

290. The process of claim 289, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

291. The process of claim 289, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

292. The process of claim 291, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

293. The process of claim 283, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

294. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical in part or whole to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) means for attaching one or more non-inherent universal detection targets (UDT) to a nucleic acid;

(iv) universal detection elements (UDE) which generate a signal directly or indirectly; and

(v) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes;

b) attaching said non-inherent UDTs to either the 3' ends of said nucleic acid analytes, the 5' ends of said first nucleic acid analytes, or both said 3' ends and said 5' ends of said nucleic acid analytes;

c) synthesizing one or more first nucleic acid copies of said nucleic acid analytes;

d) hybridizing said first nucleic acid copies with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

e) contacting said UDEs with said UDTs of said first nucleic acid copies to form a complex bound to said array; and

f) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

295. The process of claim 294, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

296. The process of claim 295, wherein said analogs comprise PNA.

297. The process of claims 295 or 296, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

298. The process of claim 294, wherein said solid support is porous or non-porous.

299. The process of claim 298, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

300. The process of claim 298, wherein said non-porous solid support comprises glass or plastic.

301. The process of claim 294, wherein said solid support is transparent, translucent, opaque or reflective.

302. The process of claim 294, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

303. The process of claim 302, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

304. The process of claim 294, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

305. The process of claim 294, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

306. The process of claim 294, wherein said attaching means add homopolymeric sequences through an enzyme selected from the group consisting of poly A polymerase and terminal transferase.

307. The process of claim 294, wherein said attaching means add homopolymeric or heteropolymeric sequences through an enzyme selected from the group consisting of DNA ligase and RNA ligase.

308. The process of claim 294, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

309. The process of claim 308, wherein said analogs comprise PNA.

310. The process of claim 294, wherein said UDE generates a signal directly or indirectly.

311. The process of claim 310, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

312. The process of claim 310, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

313. The process of claim 312, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

314. The process of claim 294, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

315. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical in part or whole to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) means for attaching one or more non-inherent universal detection targets (UDT) to a nucleic acid;

(iv) universal detection elements (UDE) which generate a signal directly or indirectly; and

(v) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes;

b) attaching said non-inherent UDTs to either the 3' ends of said nucleic acid analytes, the 5' ends of said first nucleic acid analytes, or both said 3' ends and said 5' ends of said nucleic acid analytes;

c) synthesizing one or more first nucleic acid copies of said nucleic acid analytes;

d) contacting said UDEs with said UDTs of said first nucleic acid copies to form complexes;

e) hybridizing said first nucleic acid copies with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

f) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

316. The process of claim 315, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

317. The process of claim 316, wherein said analogs comprise PNA.

318. The process of claims 316 or 317, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

319. The process of claim 315, wherein said solid support is porous or non-porous.

320. The process of claim 319, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

321. The process of claim 319, wherein said non-porous solid support comprises glass or plastic.

322. The process of claim 315, wherein said solid support is transparent, translucent, opaque or reflective.

323. The process of claim 315, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

324. The process of claim 323, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

325. The process of claim 315, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

326. The process of claim 315, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

327. The process of claim 315, wherein said attaching means add homopolymeric sequences through an enzyme selected from the group consisting of poly A polymerase and terminal transferase.

328. The process of claim 315, wherein said attaching means add homopolymeric or heteropolymeric sequences through an enzyme selected from the group consisting of DNA ligase and RNA ligase.

329. The process of claim 315, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

330. The process of claim 329, wherein said analogs comprise PNA.

331. The process of claim 315, wherein said UDE generates a signal directly or indirectly.

332. The process of claim 331, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

333. The process of claim 331, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

334. The process of claim 333, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

335. The process of claim 315, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

336. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical in part or whole to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) means for attaching one or more non-inherent universal detection targets (UDT) to a nucleic acid;

(iv) universal detection elements (UDE) which generate a signal directly or indirectly; and

(v) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes;

b) synthesizing one or more first nucleic acid copies of said nucleic acid analytes;

c) attaching said non-inherent UDTs to either the 3' ends of said first nucleic acid copies, the 5' ends of said first nucleic acid copies, or both said 3' ends and said 5' ends of said first nucleic acid copies;

d) hybridizing said first nucleic acid copies with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present;

e) contacting said UDEs with said UDTs of said first nucleic acid copies to form a complex bound to said array;

f) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

337. The process of claim 336, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

338. The process of claim 337, wherein said analogs comprise PNA.

339. The process of claims 337 or 338, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

340. The process of claim 336, wherein said solid support is porous or non-porous.

341. The process of claim 340, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

342. The process of claim 340, wherein said non-porous solid support comprises glass or plastic.

343. The process of claim 336, wherein said solid support is transparent, translucent, opaque or reflective.

344. The process of claim 336, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

345. The process of claim 344, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

346. The process of claim 336, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

347. The process of claim 336, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

348. The process of claim 336, wherein said attaching means add homopolymeric sequences through terminal transferase.

349. The process of claim 336, wherein said attaching means add homopolymeric or heteropolymeric sequences through an enzyme selected from the group consisting of DNA ligase and RNA ligase.

350. The process of claim 336, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

351. The process of claim 350, wherein said analogs comprise PNA.

352. The process of claim 336, wherein said UDE generates a signal directly or indirectly.

353. The process of claim 352, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

354. The process of claim 352, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

355. The process of claim 354, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

356. The process of claim 336, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

357. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical in part or whole to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) means for attaching one or more non-inherent universal detection targets (UDT) to a nucleic acid;

(iv) universal detection elements (UDE) which generate a signal directly or indirectly; and

(v) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes;

b) synthesizing one or more first nucleic acid copies of said nucleic acid analytes;

c) attaching said non-inherent UDTs to either the 3' ends of said first nucleic acid copies, the 5' ends of said first nucleic acid copies, or both said 3' ends and said 5' ends of said first nucleic acid copies;

d) contacting said UDEs with said UDTs of said first nucleic acid copies to form a complex;

e) hybridizing said first nucleic acid copies with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present; and

f) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

358. The process of claim 357, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

359. The process of claim 358, wherein said analogs comprise PNA.

360. The process of claims 358 or 359, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

361. The process of claim 357, wherein said solid support is porous or non-porous.

362. The process of claim 361, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

363. The process of claim 361, wherein said non-porous solid support comprises glass or plastic.

364. The process of claim 357, wherein said solid support is transparent, translucent, opaque or reflective.

365. The process of claim 357, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

366. The process of claim 365, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

367. The process of claim 357, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

368. The process of claim 357, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

369. The process of claim 357, wherein said attaching means add homopolymeric sequences through terminal transferase.

370. The process of claim 357, wherein said attaching means add homopolymeric or heteropolymeric sequences through an enzyme selected from the group consisting of DNA ligase and RNA ligase.

371. The process of claim 357, wherein said UDE is selected from the group consisting of nucleic acids, nucleic acid analogs and modified forms thereof.

372. The process of claim 371, wherein said analogs comprise PNA.

373. The process of claim 357, wherein said UDE generates a signal directly or indirectly.

374. The process of claim 373, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

375. The process of claim 373, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

376. The process of claim 375, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

377. The process of claim 357, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

378. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids complementary to said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) universal detection elements (UDEs) which bind to a domain for complex formation formed by nucleic acid hybrids and generate a signal directly or indirectly; and

(iv) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes;

b) synthesizing one or more nucleic acid copies of said nucleic acid analytes;

c) hybridizing said first nucleic acid copies with said array of nucleic acids (i) to form hybrids if said nucleic acids of interest are present, wherein said formed hybrids generate a domain for complex formation;

d) contacting said UDEs with said hybrids to form a complex bound to said array; and

e) detecting or quantifying said more than one nucleic acid of interest by detecting or measuring the amount of signal generated from UDEs bound to said array.

379. The process of claim 378, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

380. The process of claim 379, wherein said analogs comprise PNA.

381. The process of claims 379 or 380, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

382. The process of claim 378, wherein said solid support is porous or non-porous.

383. The process of claim 382, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

384. The process of claim 382, wherein said non-porous solid support comprises glass or plastic.

385. The process of claim 378, wherein said solid support is transparent, translucent, opaque or reflective.

386. The process of claim 378, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

387. The process of claim 386, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

388. The process of claim 378, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

389. The process of claim 378, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

390. The process of claim 378, wherein said domain for complex formation is selected from the group consisting of DNA-DNA hybrids, DNA-RNA hybrids, RNA-RNA hybrids, DNA-PNA hybrids and RNA-PNA hybrids.

391. The process of claim 378, wherein said signaling entity complexed to said domain is selected from the group consisting of proteins and intercalators.

392. The process of claim 391, wherein said proteins comprise nucleic acid binding proteins which bind preferentially to double-stranded nucleic acid.

393. The process of claim 392, wherein said nucleic acid binding proteins comprise antibodies.

394. The process of claim 393, wherein said antibodies are specific for nucleic acid hybrids selected from the group consisting of DNA-DNA hybrids, DNA-RNA hybrids, RNA-RNA hybrids, DNA-PNA hybrids and RNA-PNA hybrids

395. The process of claim 391, wherein said intercalators are selected from the group consisting of ethidium bromide, diethidium bromide, acridine orange and SYBR Green.

396. The process of claim 391, wherein said protein generates a signal directly or indirectly.

397. The process of claim 396, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

398. The process of claim 396, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

399. The process of claim 398, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

400. The process of claim 378, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

401. A composition of matter comprising a library of double-stranded nucleic acids substantially incapable of in vivo replication and free of non-inherent homopolymeric sequences, said nucleic acids comprising sequences complementary or identical in part or whole to inherent sequences of a library obtained from a sample, wherein said double-stranded nucleic acids comprise at least one inherent universal detection target (UDT) proximate to one end of said double strand and at least one non-inherent production center proximate to the other end of said double strand.

402. The composition of claim 401, wherein said sample comprises a biological source selected from the group consisting of organs, tissues and cells.

403. The composition of claim 401, wherein said library of nucleic acids are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

404. The composition of claim 401, wherein said inherent UDT is selected from the group consisting of 3′ polyA segments, consensus sequences, or both.

405. The composition of claim 404, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

406. The composition of claim 401, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

407. The composition of claim 406, wherein said RNA promoters comprise phage promoters.

408. The composition of claim 407, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

409. A composition of matter comprising a library of double-stranded nucleic acids substantially incapable of in vivo replication, said nucleic acids comprising sequences complementary or identical in part or whole to inherent sequences of a library obtained from a sample, wherein said double-stranded nucleic acids comprise at least four (4) non-inherent nucleotides proximate to one end of said double strand and a non-inherent production center proximate to the other end of said double strand.

410. The composition of claim 409, wherein said sample comprises a biological source selected from the group consisting of organs, tissues and cells.

411. The composition of claim 409, wherein said library of nucleic acids are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

412. The composition of claim 409, further comprising one or more inherent UDTs selected from the group consisting of 3′ polyA segments, consensus sequences, or both.

413. The composition of claim 412, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

414. The composition of claim 409, wherein said at least four (4) non-inherent nucleotides are homopolymeric.

415. The composition of claim 409, wherein said non-inherent production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

416. The composition of claim 415, wherein said RNA promoters comprise phage promoters.

417. The composition of claim 416, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

418. A composition of matter comprising a library of double-stranded nucleic acids fixed to a solid support, said nucleic acids comprising sequences complementary or identical in part or whole to inherent sequences of a library obtained from a sample and said nucleic acids further comprising at least one first sequence segment of non-inherent nucleotides proximate to one end of said double strand and at least one second sequence segment proximate to the other end of said double strand,

said second sequence segment comprising at least one production center.

419. The composition of claim 418, wherein said solid support comprises beads.

420. The composition of claim 419, wherein said beads are magnetic.

421. The composition of claim 418, wherein said sample comprises a biological source selected from the group consisting of organs, tissues and cells.

422. The composition of claim 418, wherein said library of nucleic acids are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

423. The composition of claim 418, further comprising one or more inherent UDTs selected from the group consisting of 3′ poly A segments, consensus sequences, or both.

424. The composition of claim 423, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

425. The composition of claim 418, wherein said non-inherent production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

426. The composition of claim 425, wherein said RNA promoters comprise phage promoters.

427. The composition of claim 426, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

428. A composition of matter comprising a library of double-stranded nucleic acids attached to a solid support, said nucleic acids comprising sequences complementary or identical in part or whole to inherent sequences of a library obtained from a sample, wherein said double-stranded nucleic acids comprise at least one inherent universal detection target (UDT) proximate to one end of said double strand and at least one non-inherent production center proximate to the other end of said double strand.

429. The composition of claim 428, wherein said solid support comprises beads.

430. The composition of claim 429, wherein said beads are magnetic.

431. The composition of claim 428, wherein said sample comprises a biological source selected from the group consisting of organs, tissues and cells.

432. The composition of claim 428, wherein said library of nucleic acids are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

433. The composition of claim 428, wherein said inherent UDT is selected from the group consisting of 3' polyA segments, consensus sequences, or both.

434. The composition of claim 433, wherein said consensus sequences is selected from the group consisting of signal sequences for polyA addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

435. The composition of claim 428, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

436. The composition of claim 435, wherein said RNA promoters comprise phage promoters.

437. The composition of claim 436, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

438. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified; and

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers and a second set of primers, wherein said second set of primers comprises at least two segments, the first segment at the 3' end comprising random sequences, and the second segment comprising at least one production center;

(iv) means for synthesizing nucleic acid copies under isothermal or isostatic conditions;

b) contacting said library of nucleic acid analytes with said first set of

primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) contacting said extended first copies with said second set of primers to form more than one second bound entity;

e) extending said bound second set of primers by means of template sequences provided by said extended first copies to form more than one complex comprising extended first copies and extended second set of primers;

f) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

g) hybridizing said nucleic acid copies formed in step f) to said array of nucleic acids provided in step a) (i); and

h) detecting or quantifying any of said hybridized copies obtained in step g).

439. The process of claim 438, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

440. The process of claim 439, wherein said analogs comprise PNA.

441. The process of claims 439 or 440, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

442. The process of claim 438, wherein said nucleic acid array is fixed or immobilized to a solid support.

443. The process of claim 442, wherein said solid support is porous or non-porous.

444. The process of claim 443, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

445. The process of claim 443, wherein said non-porous solid support comprises glass or plastic.

446. The process of claim 442, wherein said solid support is transparent, translucent, opaque or reflective.

447. The process of claim 442, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

448. The process of claim 447, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

449. The process of claim 438, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

450. The process of claim 438, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

451. The process of claim 438, wherein said first set of primers are complementary to inherent UDTs.

452. The process of claim 438, wherein said inherent UDT is selected from the group consisting of 3′ poly A segments, consensus sequences, and a combination of both.

453. The process of claim 452, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

454. The process of claim 438, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

455. The process of claim 454, wherein said RNA promoters comprise phage promoters.

456. The process of claim 455, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

457. The process of claim 438, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

458. The process of claim 457, wherein said signaling entities generate a signal directly or indirectly.

459. The process of claim 458, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

460. The process of claim 458, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

461. The process of claim 460, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

462. The process of claim 438, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

463. The process of claim 438, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

464. The process of claim 438, wherein step g) is carried out repeatedly.

465. The process of claim 438, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse

transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

466. The process of claim 438, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

467. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers and a second set of primers, wherein said first set of primers comprise at least one production center; and

(iv) means for synthesizing nucleic acid copies under isothermal or isostatic conditions;

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) extending said first copies by means of at least four (4) or more non-

inherent homopolymeric nucleotides;

e) contacting said extended first copies with said second set of primers to form more than one second bound entity;

f) extending said bound second set of primers by means of template sequences provided by said extended first copies to form more than one complex comprising extended first copies and extended second set of primers;

g) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

h) hybridizing said nucleic acid copies formed in step g) to said array of nucleic acids provided in step a) (i); and

i) detecting or quantifying any of said hybridized copies obtained in step h).

468. The process of claim 467, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

469. The process of claim 468, wherein said analogs comprise PNA.

470. The process of claims 468 or 469, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

471. The process of claim 467, wherein said nucleic acid array is fixed or immobilized to a solid support.

472. The process of claim 471, wherein said solid support is porous or non-porous.

473. The process of claim 472, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

474. The process of claim 472, wherein said non-porous solid support comprises glass or plastic.

475. The process of claim 471, wherein said solid support is transparent, translucent, opaque or reflective.

476. The process of claim 471, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

477. The process of claim 471, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

478. The process of claim 467, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

479. The process of claim 467, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

480. The process of claim 467, wherein said first set of primers further comprise one or more sequences complementary to inherent universal detection targets' (UDTs).

481. The process of claim 467, wherein said inherent UDT is selected from the group consisting of 3′ poly A segments, consensus sequences, and a combination of both.

482. The process of claim 481, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

483. The process of claim 467, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

484. The process of claim 483, wherein said RNA promoters comprise phage promoters.

485. The process of claim 484, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

486. The process of claim 467, wherein said extending step d), the four or more non-inherent homopolymeric nucleotides are added by terminal transferase.

487. The process of claim 467, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

488. The process of claim 487, wherein said signaling entities generate a signal directly or indirectly.

489. The process of claim 488, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

490. The process of claim 489, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

491. The process of claim 490, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

492. The process of claim 467, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

493. The process of claim 467, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

494. The process of claim 467, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

495. The process of claim 467, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

496. The process of claim 467, wherein step g) is carried out repeatedly.

497. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers and a second set of primers, wherein said first set comprises at least one production center;

(iv) a set of oligonucleotides or polynucleotides complementary to at least one segment or sequence of said second set of primers;

and (v) means for ligating said set of oligonucleotides or polynucleotides (iv);

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) ligating said set of oligonucleotides or polynucleotides a) (iv) to the 3' end of said first copies formed in step c) to form more than one ligated product;

e) contacting said ligated product with said second set of primers to form more than one second bound entity;

f) extending said bound second set of primers by means of template sequences provided by said ligated products formed in step d) to form more than one complex comprising said ligated products and said extended second set of primers;

g) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

h) hybridizing said nucleic acid copies formed in step g) to said array of nucleic acids provided in step a) (i); and

i) detecting or quantifying any of said hybridized copies obtained in step h).

498. The process of claim 497, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

499. The process of claim 498, wherein said analogs comprise PNA.

500. The process of claims 498 or 499, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

501. The process of claim 497, wherein said nucleic acid array is fixed or immobilized to a solid support.

502. The process of claim 501, wherein said solid support is porous or non-porous.

503. The process of claim 502, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

504. The process of claim 502, wherein said non-porous solid support comprises glass or plastic.

505. The process of claim 501, wherein said solid support is transparent, translucent, opaque or reflective.

506. The process of claim 501, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

507. The process of claim 506, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

508. The process of claim 497, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

509. The process of claim 497, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

510. The process of claim 497, wherein said first set of primers are complementary to inherent universal detection targets (UDTs).

511. The process of claim 497, wherein said inherent UDTs are selected from the group consisting of 3' poly A segments, consensus sequences, and a combination of both.

512. The process of claim 511, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

513. The process of claim 497, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

514. The process of claim 513, wherein said RNA promoters comprise phage promoters.

515. The process of claim 514, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

516. The process of claim 497, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporate thereto.

517. The process of claim 516, wherein said signaling entities generate a signal directly or indirectly.

518. The process of claim 517, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

519. The process of claim 517, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

520. The process of claim 519, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

521. The process of claim 497, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

522. The process of claim 497, wherein said ligating means comprise T4 DNA ligase.

523. The process of claim 497, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

524. The process of claim 497, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

525. The process of claim 497, wherein step g) is carried out repeatedly.

526. The process of claim 497, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

527. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first

set of primers and a second set of primers, wherein said second set comprises at least one production center;

(iv) a set of oligonucleotides or polynucleotides complementary to at least one segment or sequence of said second set of primers;

and (v) means for ligating said set of oligonucleotides or polynucleotides (iv);

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) ligating said set of oligonucleotides or polynucleotides a) (iv) to the 3' end of said first copies formed in step c) to form more than one ligated product;

e) contacting said ligated product with said second set of primers to form more than one second bound entity;

f) extending said bound second set of primers by means of template sequences provided by said ligated products formed in step d) to form more than one complex comprising said ligated products and said extended second set of primers;

g) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

h) hybridizing said nucleic acid copies formed in step g) to said array of nucleic acids provided in step a) (i); and

i) detecting or quantifying any of said hybridized copies obtained in step h).

528. The process of claim 527, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

529. The process of claim 528, wherein said analogs comprise PNA.

530. The process of claims 528 or 529, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

531. The process of claim 527, wherein said nucleic acid array is fixed or immobilized to a solid support.

532. The process of claim 531, wherein said solid support is porous or non-porous.

533. The process of claim 532, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

534. The process of claim 532, wherein said non-porous solid support comprises glass or plastic.

535. The process of claim 531, wherein said solid support is transparent, translucent, opaque or reflective.

536. The process of claim 531, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

537. The process of claim 536, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

538. The process of claim 527, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

539. The process of claim 527, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

540. The process of claim 527, wherein said first set of primers comprise one or more sequences which are complementary to inherent universal detection targets (UDTs).

541. The process of claim 527, wherein said inherent UDTs are selected from the group consisting of 3′ poly A segments, consensus sequences, and a combination of both.

542. The process of claim 541, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

543. The process of claim 527, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

544. The process of claim 543, wherein said RNA promoters comprise phage promoters.

545. The process of claim 544, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

546. The process of claim 527, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

547. The process of claim 546, wherein said signaling entities generate a signal directly or indirectly.

548. The process of claim 547, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

549. The process of claim 547, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

550. The process of claim 549, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

551. The process of claim 527, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse

transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

552. The process of claim 527, wherein said ligating means comprise T4 DNA ligase.

553. The process of claim 527, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

554. The process of claim 527, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

555. The process of claim 527, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

556. The process of claim 527, wherein step g) is carried out repeatedly.

557. The process of claim 527, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

558. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified; and

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers, a second set of primers and a third set of primers wherein said third set comprises at least one production center; and

b) contacting said library of nucleic acid analytes with said first set of primers to form a first set of bound primers;

c) extending said first set of bound primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) contacting said extended first copies with said second set of primers to form a second set of bound primers;

e) extending said second set of bound primers by means of template sequences provided by said extended first copies to form second copies of said nucleic acid analytes;

f) contacting said second copies with said third set of primers to form more than one third bound entity to form a third set of bound primers;

g) extending said third set of bound primers by means of template sequences provided by said extended second set of primers to form a hybrid comprising a second copy, a third copy and at least one production center;

h) synthesizing from said production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

i) hybridizing said nucleic acid copies formed in step i) to said array of nucleic acids provided in step a) (i); and

j) detecting or quantifying any of said hybridized copies obtained in step i).

559. The process of claim 558, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

560. The process of claim 559, wherein said analogs comprise PNA.

561. The process of claims 559 or 560, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

562. The process of claim 558, wherein said nucleic acid array is fixed or immobilized to a solid support.

563. The process of claim 562, wherein said solid support is porous or non-porous.

564. The process of claim 563, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

565. The process of claim 563, wherein said non-porous solid support comprises glass or plastic.

566. The process of claim 562, wherein said solid support is transparent, translucent, opaque or reflective.

567. The process of claim 562, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

568. The process of claim 562, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

569. The process of claim 558, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

570. The process of claim 558, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

571. The process of claim 558, wherein said first set of primers comprise one or more sequences which are complementary to inherent universal detection targets (UDTs).

572. The process of claim 558, wherein said inherent UDTs are selected from the group consisting of 3' poly A segments, consensus sequences, and a combination of both.

573. The process of claim 572, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

574. The process of claim 558, wherein said second set of primers are random primers.

575. The process of claim 558, further comprising the step c') of adding a primer binding site after step c).

576. The process of claim 575, wherein said second set of primers are complementary to said primer binding site.

577. The process of claim 575, wherein said primer binding site is added by means of T4 DNA ligase or terminal transferase.

578. The process of claim 558, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

579. The process of claim 578, wherein said RNA promoters comprise phage promoters.

580. The process of claim 579, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

581. The process of claim 558, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

582. The process of claim 581, wherein said signaling entities generate a signal directly or indirectly.

583. The process of claim 582, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

584. The process of claim 582, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

585. The process of claim 584, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

586. The process of claim 558, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

587. The process of claim 558, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

588. The process of claim 558, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

589. The process of claim 558, wherein step g) is carried out repeatedly.

590. The process of claim 558, further comprising the step f') of separating said extended second set of primers obtained in step e).

591. The process of claim 558, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

592. The process of claim 558, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

593. The process of claim 558, wherein step g) is carried out repeatedly.

594. The process of claim 558, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

595. The process of claim 594, wherein said second set of primers comprise at least one production center which differs in nucleotide sequence from said production center in the third set of primers.

596. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified; and

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers and a second set of primers, wherein said first set of primers are fixed or immobilized to a solid support, and wherein said second set of primers comprises at least two segments, the first segment at the 3' end comprising random sequences, and the second segment comprising at least one production center;

(iv) means for synthesizing nucleic acid copies under isothermal or isostatic conditions;

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) contacting said extended first copies with said second set of primers to form more than one second bound entity;

e) extending said bound second set of primers by means of template sequences provided by said extended first copies to form more than one complex comprising extended first copies and extended second set of primers;

f) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

g) hybridizing said nucleic acid copies formed in step f) to said array of nucleic acids provided in step a) (i); and

h) detecting or quantifying any of said hybridized copies obtained in step g).

597. The process of claim 596, wherein said solid support comprises beads.

598. The process of claim 597, wherein said beads are magnetic.

599. The process of claim 596, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

600. The process of claim 599, wherein said analogs comprise PNA.

601. The process of claims 599 or 600, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

602. The process of claim 596, wherein said nucleic acid array is fixed or immobilized to a solid support.

603. The process of claim 602, wherein said solid support is porous or non-porous.

604. The process of claim 603, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

605. The process of claim 603, wherein said non-porous solid support comprises glass or plastic.

606. The process of claim 602, wherein said solid support is transparent, translucent, opaque or reflective.

607. The process of claim 602, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

608. The process of claim 607, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

609. The process of claim 596, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

610. The process of claim 596, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

611. The process of claim 596, wherein said first set of primers comprise one or more sequences which are complementary to inherent universal detection targets (UDTs).

612. The process of claim 596, wherein said inherent UDTs are selected from the group consisting of 3' poly A segments, consensus sequences, and a combination of both.

613. The process of claim 612, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

614. The process of claim 596, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

615. The process of claim 614, wherein said RNA promoters comprise phage promoters.

616. The process of claim 615, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

617. The process of claim 596, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

618. The process of claim 617, wherein said signaling entities generate a signal directly or indirectly.

619. The process of claim 618, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

620. The process of claim 618, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

621. The process of claim 620, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

622. The process of claim 596, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

623. The process of claim 596, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

624. The process of claim 596, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

625. The process of claim 596, wherein step g) is carried out repeatedly.

626. The process of claim 596, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

627. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers and a second set of primers, wherein said first set of primers are fixed or immobilized to a solid support, and wherein said first set of primers comprise at least one production center; and

(iv) means for synthesizing nucleic acid copies under isothermal or isostatic conditions;

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) extending said first copies by means of at least four (4) or more non-inherent homopolymeric nucleotides;

e) contacting said extended first copies with said second set of primers to form more than one second bound entity;

f) extending said bound second set of primers by means of template sequences provided by said extended first copies to form more than one complex

comprising extended first copies and extended second set of primers;

g) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

h) hybridizing said nucleic acid copies formed in step g) to said array of nucleic acids provided in step a) (i); and

i) detecting or quantifying any of said hybridized copies obtained in step h).

628. The process of claim 627, wherein said solid support comprises beads.

629. The process of claim 628, wherein said beads are magnetic.

630. The process of claim 627, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

631. The process of claim 630, wherein said analogs comprise PNA.

632. The process of claims 630 or 631, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

633. The process of claim 627, wherein said nucleic acid array is fixed or immobilized to a solid support.

634. The process of claim 633, wherein said solid support is porous or non-porous.

635. The process of claim 634, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

636. The process of claim 634, wherein said non-porous solid support comprises glass or plastic.

637. The process of claim 633, wherein said solid support is transparent, translucent, opaque or reflective.

638. The process of claim 633, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

639. The process of claim 638, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

640. The process of claim 627, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

641. The process of claim 627, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

642. The process of claim 627, wherein said first set of primers further comprise one or more sequences complementary to inherent universal detection targets (UDTs).

643. The process of claim 627, wherein said inherent UDT is selected from the group consisting of 3' poly A segments, consensus sequences, and a combination of both.

644. The process of claim 643, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

645. The process of claim 627, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

646. The process of claim 645, wherein said RNA promoters comprise phage promoters.

647. The process of claim 646, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

648. The process of claim 627, wherein said extending step d), the four or more non-inherent homopolymeric nucleotides are added by terminal transferase.

649. The process of claim 627, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

650. The process of claim 649, wherein said signaling entities generate a signal directly or indirectly.

651. The process of claim 650, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

652. The process of claim 650, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

653. The process of claim 652, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

654. The process of claim 627, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

655. The process of claim 627, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

656. The process of claim 627, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

657. The process of claim 627, wherein step g) is carried out repeatedly.

658. The process of claim 627, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

659. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers and a second set of primers, wherein said first set of primers are fixed or immobilized to a solid support, and wherein said first set comprises at least one production center;

(iv) a set of oligonucleotides or polynucleotides complementary to at least one segment or sequence of said second set of primers;

and (v) means for ligating said set of oligonucleotides or polynucleotides (iv);

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said

analytes;

d) ligating said set of oligonucleotides or polynucleotides a) (iv) to the 3' end of said first copies formed in step c) to form more than one ligated product;

e) contacting said ligated product with said second set of primers to form more than one second bound entity;

f) extending said bound second set of primers by means of template sequences provided by said ligated products formed in step d) to form more than one complex comprising said ligated products and said extended second set of primers;

g) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

h) hybridizing said nucleic acid copies formed in step g) to said array of nucleic acids provided in step a) (i); and

i) detecting or quantifying any of said hybridized copies obtained in step h).

660. The process of claim 659, wherein said solid support comprises beads.

661. The process of claim 660, wherein said beads are magnetic.

662. The process of claim 659, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

663. The process of claim 662, wherein said analogs comprise PNA.

664. The process of claims 662 or 663, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

665. The process of claim 659, wherein said nucleic acid array is fixed or immobilized to a solid support.

666. The process of claim 665, wherein said solid support is porous or non-porous.

667. The process of claim 666, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

668. The process of claim 666, wherein said non-porous solid support comprises glass or plastic.

669. The process of claim 665, wherein said solid support is transparent, translucent, opaque or reflective.

670. The process of claim 665, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

671. The process of claim 665, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

672. The process of claim 659, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

673. The process of claim 659, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

674. The process of claim 659, wherein said first set of primers comprise one or more sequences which are complementary to inherent universal detection targets (UDTs).

675. The process of claim 659, wherein said inherent UDTs are selected from the group consisting of 3′ poly A segments, consensus sequences, and a combination of both.

676. The process of claim 675, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

677. The process of claim 659, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

678. The process of claim 677, wherein said RNA promoters comprise phage promoters.

679. The process of claim 678, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

680. The process of claim 659, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

681. The process of claim 680, wherein said signaling entities generate a signal directly or indirectly.

682. The process of claim 681, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

683. The process of claim 682, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

684. The process of claim 683, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

685. The process of claim 659, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

686. The process of claim 659, wherein said ligating means comprise T4 DNA ligase.

687. The process of claim 659, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

688. The process of claim 659, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

689. The process of claim 659, wherein step g) is carried out repeatedly.

690. The process of claim 659, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

691. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers and a second set of primers, wherein said first set of primers are fixed or immobilized to a solid support, and wherein said second set comprises at least one production center;

(iv) a set of oligonucleotides or polynucleotides complementary to at least one segment or sequence of said second set of primers;

and (v) means for ligating said set of oligonucleotides or polynucleotides (iv);

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) ligating said set of oligonucleotides or polynucleotides a) (iv) to the 3' end of said first copies formed in step c) to form more than one ligated product;

e) contacting said ligated product with said second set of primers to form more than one second bound entity;

f) extending said bound second set of primers by means of template sequences provided by said ligated products formed in step d) to form more than one complex comprising said ligated products and said extended second set of primers;

g) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

h) hybridizing said nucleic acid copies formed in step g) to said array of nucleic acids provided in step a) (i); and

i) detecting or quantifying any of said hybridized copies obtained in step h).

692. The process of claim 691, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

693. The process of claim 691, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

694. The process of claim 691, wherein step g) is carried out repeatedly.

695. The process of claim 691, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

696. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of fixed or immobilized nucleic acids identical or complementary in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified; and

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes, said polymerizing means comprising a first set of primers, a second set of primers and a third set of primers, wherein said first set of primers are fixed or immobilized to a solid support, and wherein said third set comprises at least one production center; and

b) contacting said library of nucleic acid analytes with said first set of primers to form more than one first bound entity;

c) extending said bound first set of primers by means of template

sequences provided by said nucleic acid analytes to form first copies of said analytes;

d) contacting said extended first copies with said second set of primers to form more than one second bound entity;

e) extending said bound second set of primers by means of template sequences provided by said extended first copies to form an extended second set of primers;

f) separating said extended second set of primers obtained in step e)

g) contacting said extended second set of primers with said third set of primers to form more than one third bound entity;

h) extending said third bound entity by means of template sequences provided by said extended second set of primers to form more than one complex comprising said extended third bound entity and said extended set of primers;

i) synthesizing from a production center in said second set of primers in said complexes one or more nucleic acid copies under isothermal or isostatic conditions;

j) hybridizing said nucleic acid copies formed in step i) to said array of nucleic acids provided in step a) (i); and

k) detecting or quantifying any of said hybridized copies obtained in step j).

697. The process of claim 696, wherein said solid support comprises beads.

698. The process of claim 697, wherein said beads are magnetic.

699. The process of claim 696, wherein said nucleic acid array comprises members selected from the group consisting of DNA, RNA and analogs thereof.

700. The process of claim 699, wherein said analogs comprise PNA.

701. The process of claims 699 or 700, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

702. The process of claim 696, wherein said nucleic acid array is fixed or immobilized to a solid support.

703. The process of claim 702, wherein said solid support is porous or non-porous.

704. The process of claim 703, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

705. The process of claim 703, wherein said non-porous solid support comprises glass or plastic.

706. The process of claim 703, wherein said solid support is transparent, translucent, opaque or reflective.

707. The process of claim 703, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

708. The process of claim 707, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

709. The process of claim 696, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

710. The process of claim 696, wherein said library of nucleic acids analytes are derived from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

711. The process of claim 696, wherein said first set of primers comprise one or more sequences which are complementary to inherent universal detection targets (UDTs).

712. The process of claim 696, wherein said inherent UDTs are selected from the group consisting of 3′ poly A segments, consensus sequences, and a combination of both.

713. The process of claim 712, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

714. The process of claim 696, wherein said second set of primers are random primers.

715. The process of claim 696, further comprising the step c') of adding a primer binding site after step c).

716. The process of claim 715, wherein said second set of primers are complementary to said primer binding site.

717. The process of claim 715, wherein said primer binding site is added by means of T4 DNA ligase or terminal transferase.

718. The process of claim 696, wherein said production center is selected from the group consisting of primer binding sites, RNA promoters, or a combination of both.

719. The process of claim 718, wherein said RNA promoters comprise phage promoters.

720. The process of claim 719, wherein said phage promoters are selected from the group consisting of T3, T7 and SP6.

721. The process of claim 696, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

722. The process of claim 721, wherein said signaling entities generate a signal directly or indirectly.

723. The process of claim 722, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

724. The process of claim 722, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

725. The process of claim 724, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

726. The process of claim 696, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

727. The process of claim 696, further comprising the step of separating the first copies obtained from step c) from their templates and repeating step b).

728. The process of claim 696, further comprising the step of separating the extended second set of primers obtained from step f) from their templates and repeating step e).

729. The process of claim 696, wherein step g) is carried out repeatedly.

730. The process of claim 696, wherein said means for synthesizing nucleic acid copies under isothermal or isostatic conditions is carried out by one or more members selected from the group consisting of RNA transcription, strand displacement amplification and secondary structure amplification.

731. The process of claim 696, wherein said second set of primers comprise at least one production center which differs in nucleotide sequence from said production center in the third set of primers.

732. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing

(i) an array of fixed or immobilized nucleic acids identical in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified; and

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes said polymerizing means comprising a first set of primers;

b) contacting said nucleic acid analytes with said first set of primers to form a first bound entity;

c) extending said bound set of first set of primers by means of template sequences provided by said nucleic acid analytes to form first nucleic acid copies of said analytes;

d) separating said first nucleic acid copies from the said analytes;

e) repeating steps b), c) and d) until a desirable amount of first nucleic acid copies have been synthesized;

f) hybridizing said nucleic nucleic acid copies formed in step e) to said array of nucleic acids provided in step (i); and

g) detecting or quantifying any of said hybridized first nucleic acid copies obtained in step f).

733. The process of claim 732, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

734. The process of claim 4, wherein said analogs comprise PNA.

735. The process of claims 733 or 734, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

736. The process of claim 732, wherein said array of nucleic acids are fixed or immobilized to a solid support.

737. The process of claim 736, wherein said solid support is porous or non-porous.

738. The process of claim 737, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

739. The process of claim 736, wherein said non-porous solid support comprises glass or plastic.

740. The process of claim 736, wherein said solid support is transparent, translucent, opaque or reflective.

741. The process of claim 736, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

742. The process of claim 741, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

743. The process of claim 732, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

744. The process of claim 732, wherein said nucleic acid analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

745. The process of claim 732, wherein said nucleic acid analytes comprise an inherent UDT selected from the group consisting of poly T segments, secondary structures, consensus sequences, and a combination of any of the foregoing.

746. The process of claim 745, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

747. The process of claim 732, further comprising the step of adding one or more non-inhererent UDTs to said nucleic acid analytes or said first copies by an enzymatic means selected from the group consisting of poly A polymerase, terminal transferase, T4 DNA ligase, T4 RNA ligase and a combination of any of the foregoing.

748. The process of claim 732, wherein said providing or contacting steps, the first set of primers comprise one or more UDTs.

749. The process of claim 732, wherein said polymerizing means comprises an enzyme selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

750. The process of claim 749, wherein an additional amount of enzyme is added after step d) or after repeating step d).

751. The process of claim 732, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

752. The process of claim 748, wherein said UDE generates a signal directly or indirectly.

753. The process of claim 752, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

754. The process of claim 752, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

755. The process of claim 754, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

756. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing

(i) an array of fixed or immobilized nucleic acids identical in part or whole to sequences of said nucleic acids of interest;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest sought to be detected or quantified;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acid analytes said polymerizing means comprising a first set of primers and a second set of primers;

(iv) means for addition of sequences to the 3′ end of nucleic acids;

b) contacting said nucleic acid analytes with said first set of primer to form a first bound entity;

c) extending said bound set of first set of primers by means of template sequences provided by said nucleic acid analytes to form first nucleic acid copies of said analytes;

d) extending said first nucleic copies by the addition of non-template derived sequences to the 3′ end of said first nucleic acid copies

e) contacting said extended first nucleic acid copies with said second set of primers to form a second bound entity;

f) extending said bound set of second set of primers by means of template sequences provided by said extended first nucleic acid copies to form second nucleic acid copies;

g) separating said second nucleic acid copies from the extended first

nucleic acid copies;

h) repeating steps e), f) and g) until a desirable amount of second nucleic acid copies have been synthesized;

i) hybridizing said second nucleic acid copies formed in step h) to said array of nucleic acids provided in step (i); and

j) detecting or quantifying any of said hybridized second nucleic acid copies obtained in step i).

757. The process of claim 756, wherein said nucleic acid array is selected from the group consisting of DNA, RNA and analogs thereof.

758. The process of claim 757, wherein said analogs comprise PNA.

759. The process of claims 757 or 758, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

760. The process of claim 756, wherein said solid support is porous or non-porous.

761. The process of claim 760, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

762. The process of claim 760, wherein said non-porous solid support comprises glass or plastic.

763. The process of claim 758, wherein said solid support is transparent, translucent, opaque or reflective.

764. The process of claim 756, wherein said nucleic acids are directly or indirectly fixed or immobilized to said solid support.

765. The process of claim 764, wherein said nucleic acids are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

766. The process of claim 758, wherein said library of nucleic acid analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

767. The process of claim 758, wherein said nucleic acid analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

768. The process of claim 758, wherein said nucleic acid analytes comprise an inherent UDT selected from the group consisting of poly T segments, secondary structures, consensus sequences, and a combination of any of the foregoing.

769. The process of claim 768, wherein said consensus sequences is selected from the group consisting of signal sequences for poly A addition, splicing elements, multicopy repeats, and a combination of any of the foregoing.

770. The process of claim 758, further comprising the step of adding one or more non-inhererent UDTs to said nucleic acid analytes, said first copies or said second copies by an enzymatic means selected from the group consisting of poly A polymerase, terminal transferase, T4 DNA ligase, T4 RNA ligase and a combination of any of the foregoing.

771. The process of claim 758, wherein said providing or contacting steps, the first set of primers or the second set of primers or both comprise one or more UDTs.

772. The process of claim 758, wherein said extending step d) is carried out by an enzymatic means selected from the group consisting of terminal transferase, T4 DNA ligase, T4 RNA ligase, and a combination of any of the foregoing.

773. The process of claim 758, wherein said polymerizing means comprises an enzyme selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

774. The process of claim 773, wherein following one or more separation steps an additional amount of enzyme is added.

775. The process of claim 758, wherein said hybridized nucleic acid copies further comprise one or more signaling entities attached or incorporated thereto.

776. The process of claim 775, wherein said signaling entities generate a signal directly or indirectly.

777. The process of claim 776, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

778. The process of claim 776, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

779. The process of claim 778, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

780. The process of claim 756, which comprises the additional steps of k) separating the first nucleic copies produced in step c) of claim 1750 from said analytes l) repeating steps b) c) and k) until a desirable amount of first nucleic acid copies have been synthesized

781. The process of claim 756, which comprises the additional steps of l) separating the extended first nucleic copies produced in step d) of claim 1750 from said analytes and m) repeating steps b), c), d) and l) until a desirable amount of extended first nucleic acid copies have been synthesized.

782. The process of claim 756, wherein said first set of primers are attached to a solid support.

783. The process of claim 782, wherein said solid support comprises beads.

784. The process of claim 783, wherein said beads are magnetic.

785. A composition of matter that comprises

an array of solid surfaces comprising discrete areas;

wherein at least two of said discrete areas each comprises:

a first set of nucleic acid primers; and
a second set of nucleic acid primers;

wherein the nucleotide sequences in said first set of nucleic acid primers are different from the nucleotide sequences in said second set of nucleic acid primers;

wherein the nucleotide sequences of a first set of nucleic acid primers of a first discrete area and the nucleotide sequences of a first set of nucleic acid primers of a second discrete area differ from each other by at least one base; and

wherein the nucleotide sequences of the second set of nucleic acid primers of a first discrete area and the nucleotide sequences of the second set of nucleic acid primers of a second discrete area are substantially the same or identical.

786. The composition of claim 785, wherein said array of solid surfaces has been designed/synthesized such that D1 is less than D2, said D1 being the physical distance on said array between a nucleic acid primer that is part of a first set of an area and the nucleic acid primer is part of a second set of the same area, and D2 being the physical distance in a nucleic acid in a sample between the sequence of a

primer binding site in said nucleic acid in a sample for the nucleic acid primer of the first set and the complement of the primer binding site in the said nucleic acid in the sample for the nucleic acid primer in the second set.

787. The composition of claim 785, wherein said nucleic acid primers are selected from the group consisting of DNA, RNA and analogs thereof.

788. The composition of claim 787, wherein said analogs comprise PNA.

789. The composition of claims 787 or 788, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

790. The composition of claim 785, wherein said solid surfaces are porous or non-porous.

791. The composition of claim 789, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

792. The composition of claim 790, wherein said non-porous solid surfaces comprise glass or plastic.

793. The composition of claim 785, wherein said solid surfaces are transparent, translucent, opaque or reflective.

794. The composition of claim 785, wherein nucleic acid primers are directly or indirectly fixed or immobilized to said solid surfaces.

795. The composition of claim 794, wherein said nucleic acid primers are indirectly fixed or immobilized to said solid surfaces by means of a chemical linker or linkage arm.

796. A composition of matter that comprises

an array of solid surfaces comprising a plurality of discrete areas;

wherein at least two of said discrete areas each comprises:

a first set of nucleic acid primers; and
a second set of nucleic acid primers;

wherein the nucleotide sequences in said first set of nucleic acid primers are different from the nucleotide sequences in said second set of nucleic acid primers;

wherein the nucleotide sequences of a first set of nucleic acid primers of a first discrete area and the nucleotide sequences of a first set of nucleic acid primers of a second discrete area differ substantially from each other; and

wherein the nucleotide sequences of the second set of nucleic acid primers of a first discrete area and the nucleotide sequences of the second set of nucleic acid primers of a second discrete area are substantially the same or identical.

797. The composition of claim 795, wherein said array of solid surfaces has been designed/synthesized such that D1 is less than D2, said D1 being the physical distance on said array between a nucleic acid primer that is part of a first set of an area and the nucleic acid primer is part of a second set of the same area, and D2

being the physical distance in a nucleic acid in a sample between the sequence of a primer binding site in said nucleic acid in a sample for the nucleic acid primer of the first set and the complement of the primer binding site in the said nucleic acid in the sample for the nucleic acid primer in the second set.

798. The composition of claim 796, wherein said nucleic acid primers are selected from the group consisting of DNA, RNA and analogs thereof.

799. The composition of claim 798, wherein said analogs comprise PNA.

800. The composition of claims 798 or 799, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

801. The composition of claim 796, wherein said solid surfaces are porous or non-porous.

802. The composition of claim 801, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

803. The composition of claim 796, wherein said non-porous solid surfaces comprise glass or plastic.

804. The composition of claim 796, wherein said solid surfaces are transparent, translucent, opaque or reflective.

805. The composition of claim 796, wherein nucleic acid primers are directly or indirectly fixed or immobilized to said solid surfaces.

806. The composition of claim 805, wherein said nucleic acid primers are indirectly fixed or immobilized to said solid surfacees by means of a chemical linker or linkage arm.

807. A process for producing two or more copies of nucleic acids of interest in a library comprising the steps of:

a) providing:

(i) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas each comprises:

(1) a first set of nucleic acid primers; and

(2) a second set of nucleic acid primers;

wherein the nucleotide sequences in said first set of nucleic acid primers are different from the nucleotide sequences in said second set of nucleic acid primers;

wherein the nucleotide sequences of a first set of nucleic acid primers of a first discrete area and the nucleotide sequences of a first set of nucleic acid primers of a second discrete area differ from each other by at least one base; and

wherein the nucleotide sequences of the second set of nucleic acid primers of a first discrete area and the nucleotide sequences of the second set of nucleic acid primers of a second discrete area are substantially the same or identical;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acids of interest;

b) contacting a primer of said first set with a complementary sequence in said nucleic acid of interest;

c) extending said primer in the first set using said nucleic acid of interest as a template to generate an extended first primer;

d) contacting a primer in said second set with a complementary sequence in said extended first primer;

e) extending said primer in the second set using said extended first primer as a template to generate an extended second primer;

f) contacting a primer in the first set with a complementary sequence in said extended second primer;

g) extending said primer in the first set using said extended second primer as a template to generate an extended first primer; and

h) repeating steps d) through g) above one or more times.

808. The process of claim 807, wherein said nucleic acid primers are selected from the group consisting of DNA, RNA and analogs thereof.

809. The process of claim 808, wherein said analogs comprise PNA.

810. The process of claims 808 or 809, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

811. The process of claim 807, wherein said solid support is porous or non-porous.

812. The process of claim 811, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

813. The process of claim 811, wherein said non-porous solid support comprises glass or plastic.

814. The process of claim 807, wherein said solid support is transparent, translucent, opaque or reflective.

815. The process of claim 807, wherein nucleic acid primers are directly or indirectly fixed or immobilized to said solid support.

816. The process of claim 815, wherein said nucleic acid primers are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

817. The process of claim 807, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

818. The process of claim 807, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

819. The process of claim 600, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

820. A process for detecting or quantifying more than one nucleic acid of interest in a library comprising the steps of:

a) providing:

(i) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas each comprises:

(1) a first set of nucleic acid primers; and

(2) a second set of nucleic acid primers;

wherein the nucleotide sequences in said first set of nucleic acid primers are different from the nucleotide sequences in said second set of nucleic acid primers;

wherein the nucleotide sequences of a first set of nucleic acid primers of a first discrete area and the nucleotide sequences of a first set of nucleic acid primers of a second discrete area differ from each other by at least one base; and

wherein the nucleotide sequences of the second set of nucleic acid primers of a first discrete area and the nucleotide sequences of the second set of nucleic acid primers of a second discrete area are substantially the same or identical;

(ii) a library of nucleic acid analytes which may contain the nucleic acids of interest;

(iii) polymerizing means for synthesizing nucleic acid copies of said nucleic acids of interest; and

(iv) non-radioactive signal generating means capable of being attached to or incorporated into nucleic acids;

b) contacting a primer of said first set with a complementary sequence in said nucleic acid of interest;

c) extending said primer in the first set using said nucleic acid of interest as a template to generate an extended first primer;

d) contacting a primer in said second set with a complementary sequence in said extended first primer;

e) extending said primer in the second set using said extended first primer as a template to generate an extended second primer;

f) contacting a primer in the first set with a complementary sequence in said extended second primer;

g) extending said primer in the first set using said extended second primer as a template to generate an extended first primer;

h) repeating steps d) through g) above one or more times; and

i) detecting or quantifying by means of said non-radioactive signal generating means attached to or incorporated into any of said extended primers in steps c), e), g), and h).

821. The process of claim 820, wherein said nucleic acid primers are selected from the group consisting of DNA, RNA and analogs thereof.

822. The process of claim 821, wherein said analogs comprise PNA.

823. The process of claims 821 or 822, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

824. The process of claim 820, wherein said solid support is porous or non-porous.

825. The process of claim 824, wherein said porous solid support is selected from the group consisting of polyacrylamide and agarose.

826. The process of claim 824, wherein said non-porous solid support comprises glass or plastic.

827. The process of claim 820, wherein said solid support is transparent, translucent, opaque or reflective.

828. The process of claim 820, wherein nucleic acid primers are directly or indirectly fixed or immobilized to said solid support.

829. The process of claim 828, wherein said nucleic acid primers are indirectly fixed or immobilized to said solid support by means of a chemical linker or linkage arm.

830. The process of claim 820, wherein said library of analytes is derived from a biological source selected from the group consisting of organs, tissues and cells.

831. The process of claim 820, wherein said analytes are selected from the group consisting of genomic DNA, episomal DNA, unspliced RNA, mRNA, rRNA, snRNA and a combination of any of the foregoing.

832. The process of claim 820, wherein said polymerizing means are selected from the group consisting of E. coli DNA Pol I, Klenow fragment of E. coli DNA Pol I, Bst DNA polymerase, Bca DNA polymerase, Taq DNA polymerase, Tth DNA Polymerase, T4 DNA polymerase, ALV reverse transcriptase, MuLV reverse transcriptase, RSV reverse transcriptase, HIV-1 reverse transcriptase, HIV-2 reverse transcriptase, Sensiscript and Omniscript.

833. The process of claim 820, wherein said non-radioactive signal generating means are selected from the group consisting of labeled nucleotides, intercalating dyes, universal detection elements and a combination of any of the foregoing.

834. The process of claim 820, wherein said extended primers further comprise one or more signaling entities attached or incorporated thereto.

835. The process of claim 834, wherein said signaling entities generate a signal directly or indirectly.

836. The process of claim 835, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

837. The process of claim 835, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

838. The process of claim 837, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

839. A composition of matter that comprises

an array of solid surfaces comprising a plurality of discrete areas;

wherein at least two of said discrete areas comprise:

a chimeric composition comprising:

a nucleic acid portion; and

a non-nucleic acid portion;

wherein said nucleic acid portion of a first discrete area has the same sequence as the nucleic acid portion of a second discrete area; and wherein said non-nucleic acid portion has a binding affinity for analytes of interest.

840. The composition of claim 839, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

841. The composition of claim 840, wherein said analogs comprise PNA.

842. The composition of claims 840 or 841, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

843. The composition of claim 839, wherein said solid surfaces are porous or non-porous.

844. The composition of claim 843, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

845. The composition of claim 843, wherein said non-porous solid surfaces comprise glass or plastic.

846. The composition of claim 839, wherein said solid surfaces are transparent, translucent, opaque or reflective.

847. The composition of claim 839, wherein said nucleic acid portions are directly or indirectly fixed or immobilized to said solid surfaces.

848. The composition of claim 839, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

849. A composition of matter that comprises

an array of solid surfaces comprising a plurality of discrete areas;

wherein at least two of said discrete areas comprise:

a chimeric composition hybridized to complementary sequences of nucleic acids fixed or immobilized to said discrete areas, wherein said chimeric composition comprises:

a nucleic acid portion; and

a non-nucleic acid portion;

said nucleic acid portion comprising at least one sequence, wherein said non-nucleic acid portion has a binding affinity for analytes of interest, and wherein when said non-nucleic acid portion is a peptide or protein, said nucleic acid portion does not comprises sequences which are either identical or complementary to sequences that code for said peptide or protein.

850. The composition of claim 849, wherein said solid surfaces are porous or non-porous.

851. The composition of claim 850, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

852. The composition of claim 850, wherein said non-porous solid surfaces comprises glass or plastic.

853. The composition of claim 849, wherein said solid surfaces are transparent, translucent, opaque or reflective.

854. The composition of claim 849, wherein said fixed or immobilized nucleic acid is selected from the group consisting of DNA, RNA and analogs thereof.

855. The composition of claim 854, wherein said analogs comprise PNA.

856. The composition of claims 854 or 855, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

857. The composition of claim 849, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

858. The composition of claim 857, wherein said analogs comprise PNA.

859. The composition of claims 857 or 858, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

860. The composition of claim 849, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

861. A process for detecting or quantifying analytes of interest, said process comprising the steps of:

1) providing:

a) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas comprise a chimeric composition comprising a nucleic acid portion; and a non-nucleic acid portion; wherein said nucleic acid portion of a first discrete area has the same sequence as the nucleic acid portion of a second discrete area; and wherein said non-nucleic acid portion has a binding affinity for analytes of interest;

b) a sample containing or suspected of containing one or more of said analytes of interest; and

c) signal generating means;

2) contacting said array a) with the sample b) under conditions permissive of binding said analytes to said non-nucleic acid portion;

3) contacting said bound analytes with said signal generating means; and

4) detecting or quantifying the presence of said analytes.

862. The process of claim 861, wherein said solid surfaces are porous or non-porous.

863. The process of claim 862, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

864. The process of claim 862, wherein said non-porous solid surfaces comprise glass or plastic.

865. The process of claim 861, wherein said solid surfaces are transparent, translucent, opaque or reflective.

866. The process of claim 861, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

867. The process of claim 866, wherein said analogs comprise PNA.

868. The process of claims 866 or 867, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

869. The process of claim 861, wherein said nucleic acid portions are directly or indirectly fixed or immobilized to said solid surfaces.

870. The process of claim 861, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

871. The process of claim 861, wherein said signal generating means comprise direct signal generating means and indirect signal generating means.

872. The process of claim 871, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

873. The process of claim 871, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

874. The process of claim 873, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

875. A process for detecting or quantifying analytes of interest, said process comprising the steps of:

1) providing:

a) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas comprise a chimeric composition comprising a nucleic acid portion; and a non-nucleic acid portion; wherein said nucleic acid portion of a first discrete area has the same sequence as the nucleic acid portion of a second discrete area; and wherein said non-nucleic acid portion has a binding affinity for analytes of interest;

b) a sample containing or suspected of containing one or more of said analytes of interest; and

c) signal generating means;

2) labeling said analytes of interest with said signal generating means;

3) contacting said array a) with said labeled analytes under conditions permissive of binding said labeled analytes to said non-nucleic acid portion; and

4) detecting or quantifying the presence of said analytes.

876. The process of claim 875, wherein said solid surfaces are porous or non-porous.

877. The process of claim 876, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

878. The process of claim 876, wherein said non-porous solid surfaces comprise glass or plastic.

879. The process of claim 876, wherein said solid surfaces are transparent, translucent, opaque or reflective.

880. The process of claim 875, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

881. The process of claim 880, wherein said analogs comprise PNA.

882. The process of claims 880 or 881, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

883. The process of claim 875, wherein said nucleic acid portions are directly or indirectly fixed or immobilized to said solid surfaces.

884. The process of claim 875, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

885. The process of claim 875, wherein said signal generating means comprise direct signal generating means and indirect signal generating means.

886. The process of claim 885, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

887. The process of claim 885, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

888. The process of claim 887, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

889. A process for detecting or quantifying analytes of interest, said process comprising the steps of:

1) providing

a) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas comprise nucleic acids fixed or immobilized to said discrete areas,

b) chimeric compositions comprising:

i) a nucleic acid portion; and

ii) a non-nucleic acid portion;

said nucleic acid portion comprising at least one sequence, wherein said non-nucleic acid portion has a binding affinity for analytes of interest, and wherein when said non-nucleic acid portion is a peptide or protein, said nucleic acid portion does not comprise sequences which are either identical or complementary to sequences that code for said peptide or protein;

c) a sample containing or suspected of containing said analytes of interest; and

d) signal generating means;

2) contacting said array with said chimeric compositions to hybridize the nucleic acid portions of said chimeric compositions to complementary nucleic acids fixed or immobilized to said array;

3) contacting said array a) with the sample b) under conditions permissive of binding said analytes to said non-nucleic acid portion;

4) contacting said bound analytes with said signal generating means; and

5) detecting or quantifying the presence of said analytes.

890. The process of claim 889, wherein said solid surfaces are porous or non-porous.

891. The process of claim 890, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

892. The process of claim 890, wherein said non-porous solid surfaces comprises glass or plastic.

893. The process of claim 889, wherein said solid surfaces are transparent, translucent, opaque or reflective.

894. The process of claim 889, wherein said fixed or immobilized nucleic acid is selected from the group consisting of DNA, RNA and analogs thereof.

895. The process of claim 894, wherein said analogs comprise PNA.

896. The process of claims 894 or 895, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

897. The process of claim 889, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

898. The process of claim 897, wherein said analogs comprise PNA.

899. The process of claims 897 or 898, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

900. The process of claim 889, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

901. The process of claim 889, wherein said signal generating means comprise direct signal generating means and indirect signal generating means.

902. The process of claim 901, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

903. The process of claim 901, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

904. The process of claim 903, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

905. A process for detecting or quantifying analytes of interest, said process comprising the steps of:

1) providing

a) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas comprise nucleic acids fixed or immobilized to said discrete areas,

b) chimeric compositions comprising:

i) a nucleic acid portion; and

ii) a non-nucleic acid portion;

said nucleic acid portion comprising at least one sequence, wherein said non-nucleic acid portion has a binding affinity for analytes of interest, and wherein when said non-nucleic acid portion is a peptide or protein, said nucleic acid portion does not comprise sequences which are either identical or complementary to sequences that code for said peptide or protein;

c) a sample containing or suspected of containing said analytes of interest; and

d) signal generating means;

2) contacting said chimeric compositions with the sample b) under conditions permissive of binding said analytes to said non-nucleic acid portion;

3) contacting said array with said chimeric compositions to hybridize the nucleic acid portions of said chimeric compositions to complementary nucleic acids fixed or immobilized to said array;

4) contacting said bound analytes with said signal generating means; and

5) detecting or quantifying the presence of said analytes.

906. The process of claim 905, wherein said solid surfaces are porous or non-porous.

907. The process of claim 906, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

908. The process of claim 906, wherein said non-porous solid surfaces comprises glass or plastic.

909. The process of claim 905, wherein said solid surfaces are transparent, translucent, opaque or reflective.

910. The process of claim 905, wherein said fixed or immobilized nucleic acid is selected from the group consisting of DNA, RNA and analogs thereof.

911. The process of claim 910, wherein said analogs comprise PNA.

912. The process of claims 910 or 911, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

913. The process of claim 905, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

914. The process of claim 913, wherein said analogs comprise PNA.

915. The process of claims 913 or 914, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

916. The process of claim 905, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

917. The process of claim 905, wherein said signal generating means comprise direct signal generating means and indirect signal generating means.

918. The process of claim 917, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

919. The process of claim 917, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

920. The process of claim 919, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

921. A process for detecting or quantifying analytes of interest, said process comprising the steps of:

1) providing

a) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas comprise nucleic acids fixed or immobilized to said discrete areas,

b) chimeric compositions comprising:

i) a nucleic acid portion; and

ii) a non-nucleic acid portion;

said nucleic acid portion comprising at least one sequence, wherein said non-nucleic acid portion has a binding affinity for analytes of interest, and wherein when said non-nucleic acid portion is a peptide or protein, said nucleic acid portion does not comprises sequences which are either identical or complementary to sequences that code for said peptide or protein;

c) a sample containing or suspected of containing said analytes of interest; and

d) signal generating means;

2) contacting said array with said chimeric compositions to hybridize the nucleic acid portions of said chimeric compositions to complementary nucleic acids fixed or immobilized to said array;

3) labeling said analytes of interest with said signal generating means;

4) contacting said array with the labeled analytes to bind said analytes to said non-nucleic acid portion; and

5) detecting or quantifying the presence of said analytes.

922. The process of claim 921, wherein said solid surfaces are porous or non-porous.

923. The process of claim 922, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

924. The process of claim 922, wherein said non-porous solid surfaces comprises glass or plastic.

925. The process of claim 921, wherein said solid surfaces are transparent, translucent, opaque or reflective.

926. The process of claim 921, wherein said fixed or immobilized nucleic acid is selected from the group consisting of DNA, RNA and analogs thereof.

927. The process of claim 926, wherein said analogs comprise PNA.

928. The process of claims 926 or 927, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

929. The process of claim 921, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

930. The process of claim 929, wherein said analogs comprise PNA.

931. The process of claims 929 or 930, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

932. The process of claim 921, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

933. The process of claim 921, wherein said signal generating means comprise direct signal generating means and indirect signal generating means.

934. The process of claim 933, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron

dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

935. The process of claim 933, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

936. The process of claim 935, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

937. A process for detecting or quantifying analytes of interest, said process comprising the steps of:

1) providing

a) an array of solid surfaces comprising a plurality of discrete areas; wherein at least two of said discrete areas comprise nucleic acids fixed or immobilized to said discrete areas,

b) chimeric compositions comprising:

i) a nucleic acid portion; and

ii) a non-nucleic acid portion;

said nucleic acid portion comprising at least one sequence, wherein said non-nucleic acid portion has a binding affinity for analytes of interest, and wherein

when said non-nucleic acid portion is a peptide or protein, said nucleic acid portion does not comprises sequences which are either identical or complementary to sequences that code for said peptide or protein;

c) a sample containing or suspected of containing said analytes of interest; and

d) signal generating means;

2) labeling said analytes of interest with said signal generating means;

3) contacting said chimeric compositions with the labeled analytes to bind said analytes to said non-nucleic acid portion;

4) contacting said array with said chimeric compositions to hybridize the nucleic acid portions of said chimeric compositions to complementary nucleic acids fixed or immobilized to said array; and

5) detecting or quantifying the presence of said analytes.

938. The process of claim 937, wherein said solid surfaces are porous or non-porous.

939. The process of claim 938, wherein said porous solid surfaces are selected from the group consisting of polyacrylamide and agarose.

940. The process of claim 938, wherein said non-porous solid surfaces comprises glass or plastic.

941. The process of claim 937, wherein said solid surfaces are transparent, translucent, opaque or reflective.

942. The process of claim 937, wherein said fixed or immobilized nucleic acid is selected from the group consisting of DNA, RNA and analogs thereof.

943. The process of claim 942, wherein said analogs comprise PNA.

944. The process of claims 942 or 943, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

945. The process of claim 937, wherein said nucleic acid portion is selected from the group consisting of DNA, RNA and analogs thereof.

946. The process of claim 945, wherein said analogs comprise PNA.

947. The process of claims 945 or 946, wherein said nucleic acids or analogs are modified on any one of the sugar, phosphate or base moieties.

948. The process of claim 937, wherein said non-nucleic acid portions are selected from the group consisting of peptides, proteins, ligands, enzyme substrates, hormones, receptors, drugs and a combination of any of the foregoing.

949. The process of claim 937, wherein said signal generating means comprise direct signal generating means and indirect signal generating means.

950. The process of claim 949, wherein said direct signal generation is selected from the group consisting of a fluorescent compound, a phosphorescent compound, a chemiluminescent compound, a chelating compound, an electron dense compound, a magnetic compound, an intercalating compound, an energy transfer compound and a combination of any of the foregoing.

951. The process of claim 949, wherein said indirect signal generation is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a hormone, a ligand, an enzyme and a combination of any of the foregoing.

952. The process of claim 951, wherein said enzyme catalyzes a reaction selected from the group consisting of a fluorogenic reaction, a chromogenic reaction and a chemiluminescent reaction.

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